

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.
BANDMAN, Olga
TANG, Y. Tom
CORLEY, Neil C.
AZIMZAI, Yalda
BAUGHN, Mariah R.

<120> SCAD-RELATED MOLECULES

<130> PF-0559 PCT

<140> To Be Assigned
<141> Herewith

<150> 09/116,750; Unassigned
<151> 1998-07-16; 1998-07-16

<160> 6

<170> FastSEQ for Windows Version 3.0

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<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> Incyte Clone No: 1240869

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Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly Phe Ala Ile
35 40 45
Ala Arg Arg Leu Ala Gln Asp Arg Ala His Val Val Val Ser Ser Arg
50 55 60
Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr Leu Gln Gly Glu Gly
65 70 75 80
Leu Ser Val Thr Gly Thr Val Cys His Val Gly Lys Ala Glu Asp Arg
85 90 95
Glu Arg Leu Val Ala Thr Ala Val Lys Leu His Gly Gly Ile Asp Ile
100 105 110
Leu Val Ser Asn Ala Ala Val Asn Pro Phe Phe Gly Ser Ile Met Asp
115 120 125
Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala
130 135 140
Pro Ala Leu Met Thr Lys Ala Val Val Pro Glu Met Glu Lys Arg Gly
145 150 155 160
Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
165 170 175
Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
180 185 190
Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
195 200 205
Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
210 215 220

Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
 225 230 235 240
 Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
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 Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
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 Gly Thr Pro Ser Arg Leu
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<223> Incyte Clone No: 2060002

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 35 40 45
 Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
 50 55 60
 Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
 65 70 75 80
 Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
 85 90 95
 Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
 100 105 110
 Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
 115 120 125
 Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
 130 135 140
 Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
 145 150 155 160
 Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
 165 170 175
 Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
 180 185 190
 Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
 195 200 205
 Glu Glu Glu Ile Asp Phe Leu Arg Ser Asn Pro Lys Ile Trp Asn Val
 210 215 220
 His Ser Val Leu Asn Val Leu His Ser Leu Val Asp Lys Ser Asn Ile
 225 230 235 240
 Asn Arg Gln Leu Glu Val Tyr Thr Ser Gly Gly Asp Pro Glu Ser Val
 245 250 255
 Ala Gly Glu Tyr Gly Arg His Ser Leu Tyr Lys Met Leu Gly Tyr Phe
 260 265 270
 Ser Leu Val Gly Leu Leu Arg Leu His Ser Leu Leu Gly Asp Tyr Tyr
 275 280 285
 Gln Ala Ile Lys Val Leu Glu Asn Ile Glu Leu Asn Lys Lys Ser Met
 290 295 300
 Tyr Ser Arg Val Pro Glu Cys Gln Val Thr Thr Tyr Tyr Tyr Val Gly
 305 310 315 320
 Phe Ala Tyr Leu Met Met Arg Arg Tyr Gln Asp Ala Ile Arg Val Phe
 325 330 335
 Ala Asn Ile Leu Leu Tyr Ile Gln Arg Thr Lys Ser Met Phe Gln Arg
 340 345 350

Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
 355 360 365
 Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
 370 375 380
 Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
 385 390 395 400
 Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
 405 410 415
 Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
 420 425 430
 Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
 435 440 445
 Asp Glu Val Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
 450 455 460
 Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
 465 470 475 480
 Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
 485 490 495
 Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
 500 505 510
 Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
 515 520 525
 His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
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 545 550 555 560
 Gly Gln Arg Pro

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 cgtttggccc aggacagggc ccacgtggc gtcagcagcc ggaagcagca gaatgtggac 240
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Val Leu Ala Asn Arg Val Ala Val Val Thr Gly Ser Thr Ser Gly Ile
      35          40          45
Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
      50          55          60
Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
      65          70          75          80
Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
      85          90          95

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Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
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 Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
 115 120 125
 Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
 130 135 140
 Asn Val Lys Ser Pro Ala Leu Leu Ser Gln Leu Leu Pro Tyr Met
 145 150 155 160
 Glu Asn Arg Arg Gly Ala Val Ile Leu Val Ser Ser Ile Ala Ala Tyr
 165 170 175
 Asn Pro Val Val Ala Leu Gly Val Tyr Asn Val Ser Lys Thr Ala Leu
 180 185 190
 Leu Gly Leu Thr Arg Thr Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile
 195 200 205
 Arg Val Asn Cys Val Val Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys
 210 215 220
 Val Phe His Gly Asn Glu Ser Leu Trp Lys Asn Phe Lys Glu His His
 225 230 235 240
 Gln Leu Gln Arg Ile Gly Glu Ser Glu Asp Cys Ala Gly Ile Val Ser
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<213> CAENORHABDITIS ELEGANS

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 35 40 45
 Asn Val Pro Glu Ile Leu Thr Leu Tyr Asp Gln Ala Phe Pro Asp Leu
 50 55 60
 Thr Glu Arg Phe Phe Arg Asp Arg Met Trp Pro Asp Glu Asn Val Val
 65 70 75 80
 Glu Arg Ile Ile Gly Pro Gly Asn Lys Leu Phe Ile Ile Leu Tyr Lys
 85 90 95
 Glu Leu Tyr Tyr Arg Gln Leu Tyr Ala Arg Asn Thr Arg Gly Pro Leu
 100 105 110
 Leu Val His Arg Tyr Glu Ser Phe Met Asn Tyr Gln Glu Leu Phe Ser
 115 120 125
 Glu Leu Leu Ser Ser Lys Asp Pro Ile Pro Leu Ser Leu Pro Asn Val
 130 135 140
 Trp Leu Trp Asp Ile Ile Asp Glu Phe Val Tyr Gln Phe Gln Ala Phe
 145 150 155 160
 Cys Leu Tyr Lys Ala Asn Pro Gly Lys Arg Asn Ala Asp Glu Val Glu
 165 170 175
 Asp Leu Ile Asn Ile Glu Glu Asn Gln Asn Ala Trp Asn Ile Tyr Pro
 180 185 190
 Val Leu Asn Ile Leu Tyr Ser Leu Leu Ser Lys Ser Gln Ile Val Glu
 195 200 205
 Gln Leu Lys Ala Leu Lys Glu Lys Arg Asn Pro Asp Ser Val Ala Asp
 210 215 220
 Glu Phe Gly Gln Ser Asp Leu Tyr Phe Lys Leu Gly Tyr Phe Ala Leu
 225 230 235 240
 Ile Gly Leu Leu Arg Thr His Val Leu Leu Gly Asp Tyr His Gln Ala

Leu	Lys	Thr	Val	Gln	Tyr	Val	Asp	Ile	Asp	Pro	Lys	Gly	Ile	Tyr	Asn
245								250						255	
260								265						270	
Thr	Val	Pro	Thr	Cys	Leu	Val	Thr	Leu	His	Tyr	Phe	Val	Gly	Phe	Ser
275								280						285	
His	Leu	Met	Met	Arg	Asn	Tyr	Gly	Glu	Ala	Thr	Lys	Met	Phe	Val	Asn
290							295				300				
Cys	Leu	Leu	Tyr	Ile	Gln	Arg	Thr	Lys	Ser	Val	Gln	Asn	Gln	Gln	Pro
305					310					315					320
Ser	Lys	Lys	Asn	Phe	Gln	Tyr	Asp	Val	Ile	Gly	Lys	Thr	Trp	Asp	Gln
325									330						335
Leu	Phe	His	Leu	Leu	Ala	Ile	Cys	Leu	Ala	Ile	Gln	Pro	Gln	Arg	Ile
340								345						350	
Asp	Glu	Ser	Ile	Ala	Ser	Gln	Leu	Ser	Glu	Arg	Cys	Gly	Glu	Arg	Met
355								360						365	
Met	His	Met	Ala	Asn	Gly	Asn	Ile	Asp	Glu	Phe	Arg	Asn	Ala	Phe	Ala
370								375						380	
Thr	Gly	Cys	Pro	Lys	Phe	Leu	Ser	Pro	Thr	Thr	Val	Val	Tyr	Glu	Gly
385								390						395	
Val	Asn	Gln	Ser	Lys	Glu	Pro	Leu	Leu	Arg	Gln	Thr	Gln	Ser	Phe	Leu
405									410						415
Glu	Gly	Ile	Glu	Ser	Gln	Met	Ala	Leu	Pro	Val	Leu	Arg	Gly	Tyr	Leu
420									425						430
Lys	Leu	Tyr	Thr	Thr	Leu	Pro	Thr	Lys	Lys	Leu	Ala	Ser	Phe	Met	Asp
435									440						445
Val	Asp	Asp	Glu	His	Tyr	Asp	Ser	Phe	Ile	Gly	Lys	Leu	Leu	Thr	Tyr
450									455						460
Lys	Met	Ile	Val	Asn	Glu	Leu	Gly	Lys	Glu	Ala	Gly	Pro	Ser	Ser	Ala
465								470							480
Asp	Asp	Asp	Glu	Pro	Gln	Thr	Asp	Ile	Asp	Phe	Tyr	Val	Asp	Arg	Asp
485									490						495
Met	Ile	Asn	Ile	Ala	Asp	Thr	Lys	Val	Ala	Arg	His	Val	Gly	Cys	Ala
500									505						510
Gln	Thr	Thr	Arg	Tyr	Pro	Glu	Thr	Met	Ile	Leu	Lys	Lys	Lys	Phe	Val
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Gly	Arg	Thr	Val	Leu	Ile	Thr	Gly	Ala	Ser	Arg	Gly	Ile	Gly	Lys	Glu
530								535							540
Ile	Ala	Leu	Lys	Leu	Ala	Lys	Asp	Gly	Ala	Asn	Ile	Val	Val	Ala	Ala
545								550							560
Lys	Thr	Ala	Thr	Ala	His	Pro	Lys	Leu	Pro	Gly	Thr	Ile	Tyr	Ser	Ala
565									570						575
Ala	Glu	Glu	Ile	Glu	Lys	Ala	Gly	Gly	Lys	Ala	Leu	Pro	Cys	Ile	Val
580									585						590
Asp	Val	Arg	Asp	Glu	Ala	Ser	Val	Lys	Ala	Ser	Val	Glu	Glu	Ala	Val
595									600						605
Lys	Lys	Phe	Gly	Gly	Ile	Asp	Ile	Leu	Ile	Asn	Asn	Ala	Ser	Ala	Ile
610									615						620
Ser	Leu	Thr	Asp	Thr	Glu	Asn	Thr	Glu	Met	Lys	Arg	Tyr	Asp	Leu	Met
625									630						640
His	Ser	Ile	Asn	Thr	Arg	Gly	Thr	Phe	Leu	Met	Thr	Lys	Thr	Cys	Leu
645										650					655
Pro	Tyr	Leu	Lys	Ser	Gly	Lys	Asn	Pro	His	Val	Leu	Asn	Ile	Ser	Pro
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675									680						685
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690									695						700
Phe	Arg	Pro	His	Gly	Ile	Ala	Val	Asn	Ala	Leu	Trp	Pro	Leu	Thr	Ala
705									710						720
Ile	Trp	Thr	Ala	Ala	Met	Glu	Met	Leu	Ser	Asp	Lys	Gly	Gly	Glu	Ala
725									730						735
Gly	Ser	Arg	Lys	Pro	Ser	Ile	Met	Ala	Asp	Ala	Ala	Tyr	Ala	Val	Leu
740									745						750
Ser	Lys	Asn	Ser	Lys	Asp	Phe	Thr	Gly	Asn	Phe	Cys	Ile	Asp	Glu	Asp
755									760						765

Ile Leu Lys Ala Glu Gly Val Thr Asp Phe Asp Arg Tyr Ala Cys Val
770 775 780
Pro Asp Ala Pro Leu Met Pro Asp Phe Phe Ile Pro Ala Gly Thr Tyr
785 790 795 800
Asp His Lys Phe Ser Ser Gly Ala Gln Ile Gly Lys Lys Asn Lys Thr
805 810 815
His Glu Ala Gly Val Val Glu Glu Ile Lys Gln Ile Phe Thr Ser
820 825 830
Ala Lys Arg Leu Leu Asn Ala Asp Ile Val Lys Lys Thr Gly Phe Val
835 840 845
Tyr Glu Phe Leu Leu Lys Asp Pro Thr Thr Lys Ser Glu Arg Ile Ile
850 855 860
Thr Leu Asp Leu Lys Asn Gly Glu Gly Ala Leu Thr Asp Lys Lys Ala
865 870 875 880
Ser Gly Lys Ala Asp Val Lys Phe Thr Leu Ala Pro Glu His Phe Ala
885 890 895
Pro Leu Phe Thr Gly Lys Leu Arg Pro Thr Thr Ala Leu Met Thr Lys
900 905 910
Lys Leu Gln Ile Ser Gly Asp Met Pro Gly Ala Met Lys Leu Glu Ser
915 920 925
Leu Leu Arg Lys Phe Thr Glu Gly Lys Leu
930 935